

ROLE OF GENE VARIANTS IN RESISTANCE TO SMALL RUMINANT LENTIVIRUSES (SRLVs) IN FLOCKS REARED IN CENTRAL ITALY – PRELIMINARY RESULTS



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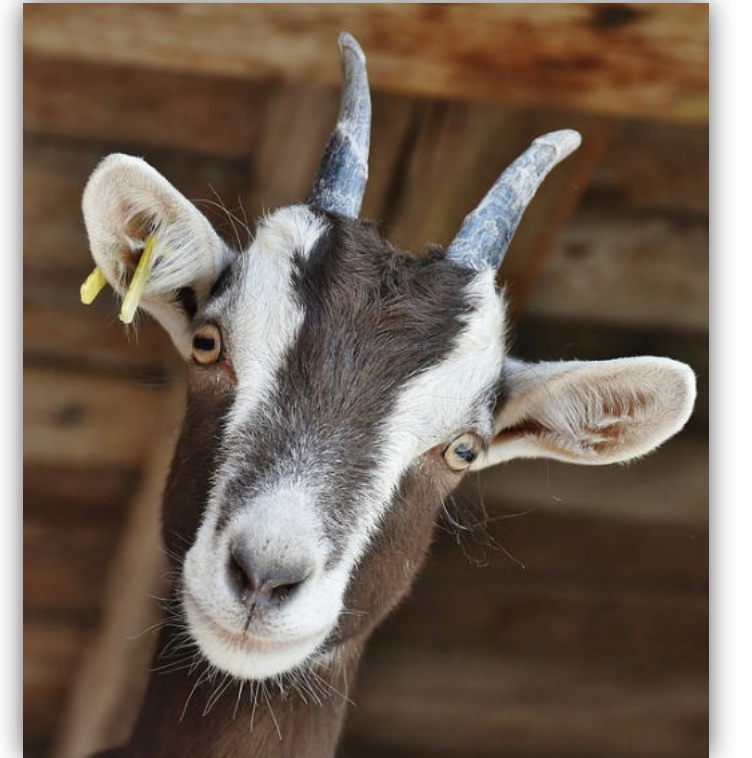
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INTRODUCTION



- **SRLVs (CAEV and MVV)** belong to the genus Lentivirus of the *Retroviridae* family;
- Infect both sheep and goats;
- Worldwide distribution with exception of Iceland;
- Affect **animal welfare** and **productions**;
- Routes of transmission: respiratory secretions and ingestion of infected colostrum/milk;
- **No vaccine or treatment.**

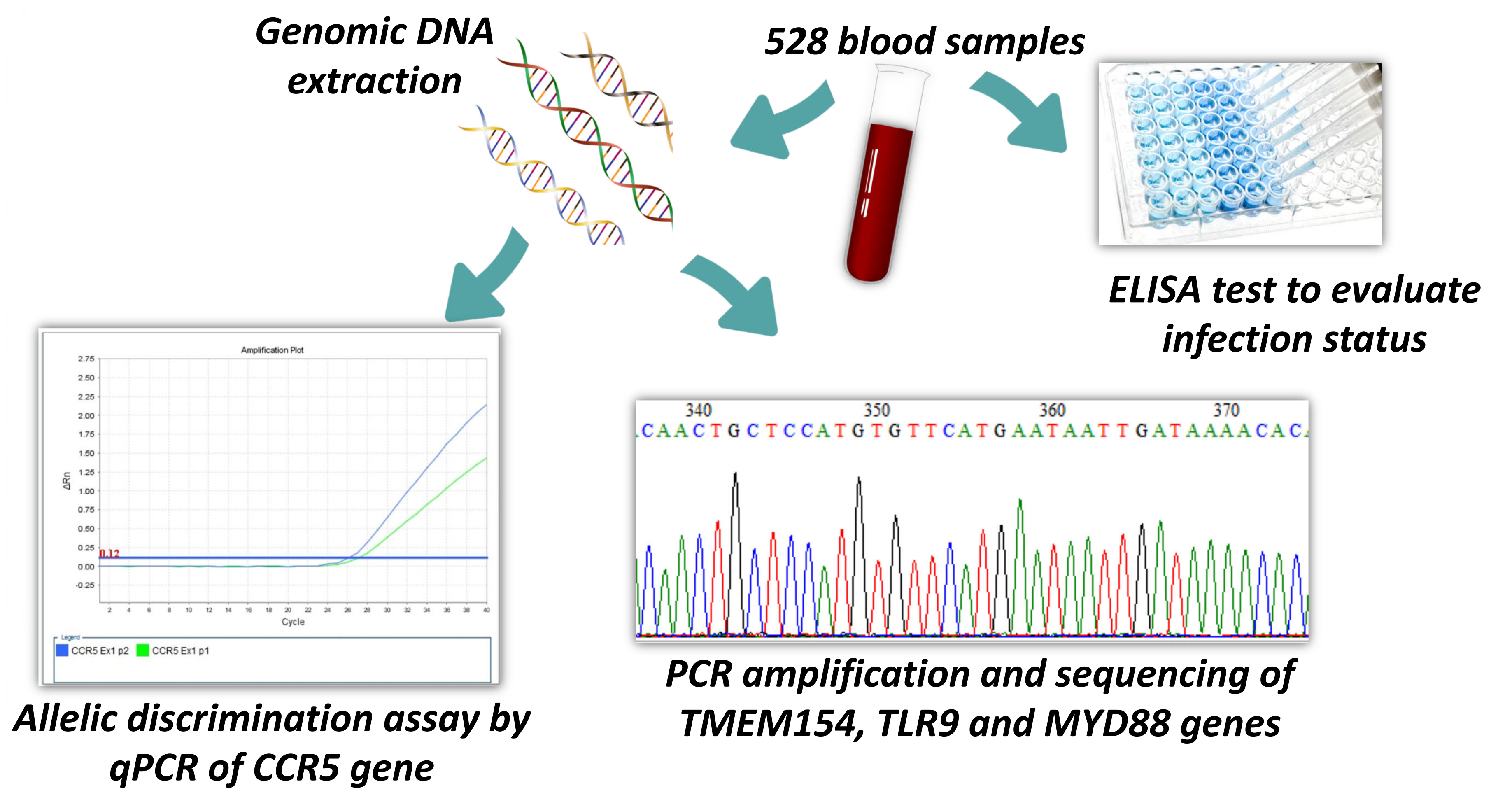
- **Genetic approach** to control the infection;
- Genes studied and involved in genetic resistance:
 - - **TMEM154** gene (E35K);
 - - **CCR5** gene (CCR5-Δ4);
 - - **TLR9** gene (G520R);
 - - **MYD88** gene polymorphisms.



AIM OF THE WORK

The aim of this work is to evaluate, for the first time, the association between **SRLVs infection** and specific variants of **TMEM154**, **CCR5**, **TLR9** and **MYD88** genes in flocks of **Central Italy**.

MATERIALS AND METHODS



RESULTS

Preliminary data showed the frequencies of already known **alleles associated with resistance to SRLVs infection**. Further investigation should be conducted to assess the presence of other polymorphisms in target genes related to resistance/susceptibility.

TMEM154 E35K		CCR5-Δ4		TLR9 G520R	
E	K	Wild type	deletion	G	R
64.8	35.2	81.2	18.2	10.7	89.3

CONCLUSIONS

The World Organization for Animal Health (OIE) has recognized the importance of the **economic impact** of SRLVs, especially on dairy sheep farms, and has included MV and CAE in the list of notifiable terrestrial and aquatic animal diseases. Identifying **genetic variants** associated with resistance to SRLVs infection could be crucial in ensuring **animal welfare** and the **profitability of farms**.

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